

Patent claims

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the citA gene, chosen from the group consisting of
- 5 a) polynucleotide which is identical to the extent of at least 70 % to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,
- 10 b) polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least to [sic] 70% to the amino acid sequence of SEQ ID No. 2,
- c) polynucleotide which is complementary to the polynucleotides of a) or b), and
- 15 d) polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b), [sic] or c),
- the polypeptide preferably having the activity of the sensor kinase CitA.
- 20 2. A polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA which is capable of replication in coryneform bacteria.
3. A polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
- 25 4. A polynucleotide as claimed in claim 2, comprising the nucleic acid sequence as shown in SEQ ID No. 1.
5. A DNA as claimed in claim 2 which is capable of replication, comprising

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- (i) the nucleotide sequence shown in SEQ ID no. 1,
or
- (ii) at least one sequence which corresponds to
sequence (i) within the range of the
degeneration of the genetic code, or
- (iii) at least one sequence which hybridizes with
the sequences complementary to sequences (i)
or (ii), and optionally
- (iv) sense mutations of neutral function in (i).
6. A process as claimed in claim 5 [sic],
wherein
the hybridization is carried out under a stringency
corresponding to at most 2x SSC.
7. A polynucleotide sequence as claimed in claim 2, which
codes for a polypeptide which comprises the amino acid
sequence shown in SEQ ID No. 2.
8. A vector pCR2.1citAint, which
- 8.1. carries an internal fragment of the citA gene
480 bp in size, shown in SEQ ID. No. 3,
- 8.2 the restriction map of which is reproduced in
figure 1, and
- 8.3 which is deposited in the E. coli strain
Top10/pCR2.1citAint at the Deutsche Sammlung für
Mikroorganismen und Zellenkulturen [German
Collection of Microorganisms and Cell Cultures]
under no. DSM 13998 [sic]
9. An internal fragment of the citA gene with a length of
480 bp, shown in SEQ ID No. 3.

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10. A coryneform bacterium, in which the citA gene is attenuated, preferably eliminated, in particular by deletion.
11. A process for the preparation of L-amino acids, in particular L-lysine,
5 w h e r e i n
 it comprises carrying out the following steps,
 a) fermentation of the coryneform bacteria which produced the desired L-amino acid and in which at least the citA gene is attenuated,
10 b) concentration of the desired product in the medium or in the cells of the bacteria and
 c) isolation of the L-amino acid.
12. A process as claimed in claim 11,
15 w h e r e i n
 bacteria in which further genes of the biosynthesis pathway of the desired L-amino acid are additionally enhanced are employed.
13. A process as claimed in claim 11,
20 w h e r e i n
 bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.
14. A process as claimed in claim 11,
25 w h e r e i n
 expression of the polynucleotide(s) which codes (code) for the citA gene is reduced, in particular eliminated.
15. A process as claimed in claim 11,
30 w h e r e i n
 the regulatory (or catalytic) properties of the polypeptide for which the polynucleotide citA codes are decreased.

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16. A process as claimed in claim 11,
w h e r e i n
for the preparation of L-amino acids, in particular L-
lysine, bacteria in which at the same time one or more
5 of the genes chosen from the group consisting of
- 16.1 the dapA gene which codes for dihydrodipicolinate
synthase,
- 16.2 the gap gene which codes for glyceraldehyde 3-
phosphate dehydrogenase
- 10 16.3 the zwf gene which codes for glucose 6-phosphate
dehydrogenase,
- 16.4 the pyc gene which codes for pyruvate
carboxylase,
- 16.5 the lysE gene which codes for lysine export,
- 15 16.6 the lysC gene which codes for a feed back
resistant aspartate kinase,
- 16.7 the zwal gene which codes for the Zwal protein
is or are enhanced, preferably over-expressed, are
fermented.
- 20 17. A process as claimed in claim 11,
w h e r e i n
at the same time one or more of the genes chosen from
the group consisting of:
- 25 17.1 the pck gene which codes for phosphoenol pyruvate
carboxykinase,
- 17.2 the pgi gene which codes for glucose 6-phosphate
isomerase,
- 17.3 the poxB gene which codes for pyruvate oxidase

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17.4 the *zwa2* gene which codes for the Zwa2 protein
is or are attenuated.

18. A process as claimed in one or more of the preceding
claims,

5 w h e r e i n
 microorganisms of the genus *Corynebacterium glutamicum*
 are employed.

19. A process for discovering RNA, cDNA and DNA in order
to isolate nucleic acids or polynucleotides or genes

10 which code for sensor kinase CitA or have a high
 similarity with the sequence of the *citA* gene,

 w h e r e i n

 it comprises employing the polynucleotides comprising
 the sequences according to claims 1 to 4 as

15 hybridization probes.

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